31. A DNA sequence of claim 12 with a nucleotide sequence homology of at least 70% with the said DNA sequence.--

REMARKS

Reconsideration of this application is requested in view of the amendments to the claims and the remarks presented herein.

The claims in the application are claims 1 to 11, 13 to 18 and 27. The non-elected claims have been cancelled but Applicants reserve the right to file a divisional application directed thereto.

The Examiner has required a seven-way restriction requirement and Applicants confirm the election of group I, namely, the claims remaining in the application.

Claims 1 to 3, 5, 8 to 11, 13 to 17 and 27 were rejected under 35 USC 112, first paragraph, as containing subject matter not adequately enabled in the specification. The Examiner stated that the claims are drawn to an isolated polynucleotide containing a polynucleotide having at least 50% similarity with a polynucleotide coding for a polypeptide with a transcription factor function and having an amino acid sequence homologous with SEQ ID No: 3 as well as DNA sequences which are that of the CatfIIIA gene coding for a protein having the biological function of a transcription factor.

The Examiner was of the opinion that only isolated polynucleotides encoding the polypeptide set forth as SEQ ID No: 3 is adequately supported by the specification.

Applicants respectfully traverse this ground of rejection since it is deemed that the claims are enabled by the specification. Claim 1 is now directed to an isolated polynucleotide containing a nucleotide sequence which has at least 50% similarity with the polynucleotide coding for a polypeptide having the function of transcription factor and an amino acid sequence of SEQ ID No: 3 which is deemed to be adequately supported by the specification and according to the Examiner. Therefore, withdrawal of this ground of rejection is requested.

Claim 18 was rejected under 35 USC 112, first paragraph, as being indefinite in the fact that it was not clear from the record that the biological material was deposited in accordance with the Budapest Treaty. Applicants wish to confirm that the biological deposit has been made in accordance with the Budapest Treaty and therefore, withdrawal of this ground of rejection is requested.

All of the claims were rejected under 35 USC 112, second paragraph, as being indefinite. The Examiner objected to the claims as not starting with an article and as being indefinite in the preferred clauses and objected to the transcription factor function.

Applicants respectfully traverse this ground of rejection since it is believed that the amended claims properly define the invention. An article has been used at the beginning of each claim and the preferred clauses have been deleted from the claims. Claim 1 in its rewritten form is believed to be free of the objections raised by the Examiner and claim 5 was amended in the preliminary amendment therefore, is believed to be free of the objections raised by the Examiner. Claim 7 has proper antecedent basis in amended claim 5 so as to obviate the Examiner's objection thereto. The same is believed to be true with respect to claim 8. "AA" has been replaced by "amino acid" and "appropriate host" no longer appears in the claims and claim 27 has been amended to delete the sequence having a similar function. Therefore, it is believed that the amended claims properly comply with 35 USC 112 and withdrawal of these grounds of rejection is requested.

Claims 1 to 3, 5, 8 to 11, 14 and 27 were rejected under 35 USC 102 as being anticipated by the Archambault et al reference and claims 1 to 3, 5, 8 to 11, 13 to 17 and 27 have been rejected under 35 USC 103 as being obvious thereover taken in view of the Fujiwara et al patent. The Examiner states that the Archambault et al reference teaches an isolated polynucleotide encoding S. cerevisiae TFIIIA which includes an amino acid sequence comprising more than 5 consecutive amino acids identical to SEQ ID No: 3 and deems that the polynucleotide comprises a polynucleotide that has at least 15 consecutive bases which encodes part of the SEQ ID No: 3 at 100%

homology. The Examiner states that the differences in the nucleic acid taught by the reference v. the claimed nucleic acids are considered to be modifications introduced by insertion, deletion and/or substitution. The Examiner concedes that the reference does not specifically teach expression of DNA sequence according to claim 5 in a host followed by isolation and purification and it does not teach host cells transformed with a vector, the host being DHS alpha E. coli or XL1-BLUE E. coli. Fujiwara et al is cited to show transformation of host cells followed by expression, isolation and purification of the protein and the Examiner deems it would be obvious to combine the same with the primary reference to overcome the deficiencies thereof.

Applicants respectfully traverse these rejections since it is deemed that the Archambault et al reference, whether taken alone or in combination with the Fujiwara et al patent, does not teach Applicants' invention. The Archambault et al reference teaches an isolated polynucleotide which encodes S. cerevisiase TFIIIA and such polynucleotide comprises more than 5 consecutive amino acids identical to SEQ ID No: 3 but the polynucleotide of Archambault et al encodes an amino acid sequence comprising some groups of 5 amino acids identical to SEQ ID No: 3 but such groups are distributed among the peptide sequence of the present application and all together, the percent of homology between the polynucleotide of Archambault et al and the polynucleotide of SEQ ID No: 3 of the present application is only 37% and is excluded from the scope of

claim 1 which requires a polynucleotide having at least 50% homology. The polypeptide of Archambault et al is therefor different from the polypeptide of the present application. Each eucaryote has such a transcription factor TFIIIA but all the sequences of the different eucaryotes such as S. cerevisiae, Candida albicans contain differences and the knowledge of one cannot predict the sequence of the others. Therefore, the sequence of Archambault et al does not define Applicants' sequence and withdrawal of the anticipation rejection is requested.

With respect to the 103 obviousness rejection, the Archambault et al reference fails for the above reasons and the citation of Fujiwara et al does not overcome the deficiencies thereof. The latter reference describes human genes and has nothing to do with fungal genes. Therefore, the sequences are completely different and Fujiwara et al could not have taught the invention of the present application which is the sequence of the gene TFIIIA of Candida albicans. Therefore, withdrawal of these grounds of rejection is requested.

In view of the amendments to the claims and the above remarks, it is believed that the claims clearly point out Applicants' patentable contribution and favorable reconsideration of the application is requested.

Respectfully submitted,
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CAM:ds
Enclosures

**MARKED UP VERSION OF CLAIMS SHOWING CHANGES MADE**

**Claim 1** (amended) An [Isolated] isolated polynucleotide containing a nucleotide sequence [chosen] selected from the [following] group consisting of:

a) a polynucleotide having at least 50% [or at least 60% and preferably at least 70%] similarity with a polynucleotide coding for a polypeptide [with an] having the function of transcription factor [function] and having an amino acid sequence [homologous with the] of sequence SEQ ID [N°.] No: 3.

**Claim 2** (amended) A [Polynucleotide] polynucleotide according to claim 1 in that this polynucleotide is a DNA.

**Claim 3** (amended) A [Polynucleotide] polynucleotide according to claim 1 in that this polynucleotide is a RNA.

**Claim 4** (amended) A [Polynucleotide] polynucleotide as defined in claim 2 comprising the nucleotide sequence SEQ ID [N°.] No: 1.

**Claim 5** (twice amended) A DNA sequence as defined in claim 1 wherein this DNA sequence is that of the CAtfIIIA gene coding for a protein having the biological function of transcription factor of Candida albicans CATFIIIA containing the nucleotide sequence SEQ ID No: 1.

**Claim 6** (amended) A DNA sequence according to claim 5 having the sequence starting at nucleotide 720 and finishing at nucleotide 1955 of SEQ ID [N°.] Nc: 1.

**Claim 7** (twice amended) A DNA sequence of the CAtfIIIA gene according to claim 5 coding for the amino acid sequence SEQ ID No:

**Claim 14** (twice amended) [Expression] An expression vector containing the DNA sequence according to claim 5.

**Claim 15** (amended) [Host] A host cell transformed with a vector according to claim 14.

**Claim 16** (amended) The process [Process as defined in] of claim 13 [in which] wherein the host cell is DH5 alpha E. coli or XL1-Blue E. coli.

**Claim 17** (amended) The process [process as defined in] of claim 13 [in which] wherein the host cell is Saccharomyces cerevisae.

**Claim 18** (twice amended) [Plasmid] The plasmid deposited at the CNCM under the number I-2072.

**Claim 27** (twice amended) Kit for the diagnosis of fungal infections comprising a DNA sequence as defined in claim 5 [or a sequence having a similar function] or a functional fragment of this sequence, the polypeptide coded by this sequence or a polypeptide fragment having the same function or an antibody directed against such a polypeptide coded by this DNA sequence or against a fragment of this polypeptide.

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| No. | Doccode | Number of pages |
|---|---|---|
| 1 | CTMS | 2 |

Total number of pages: 2

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